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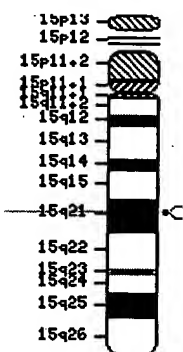
Region Shown:

57437237

57537238



☒ out  
☒ zoom  
☒ in


☒ ideogram

☐ master

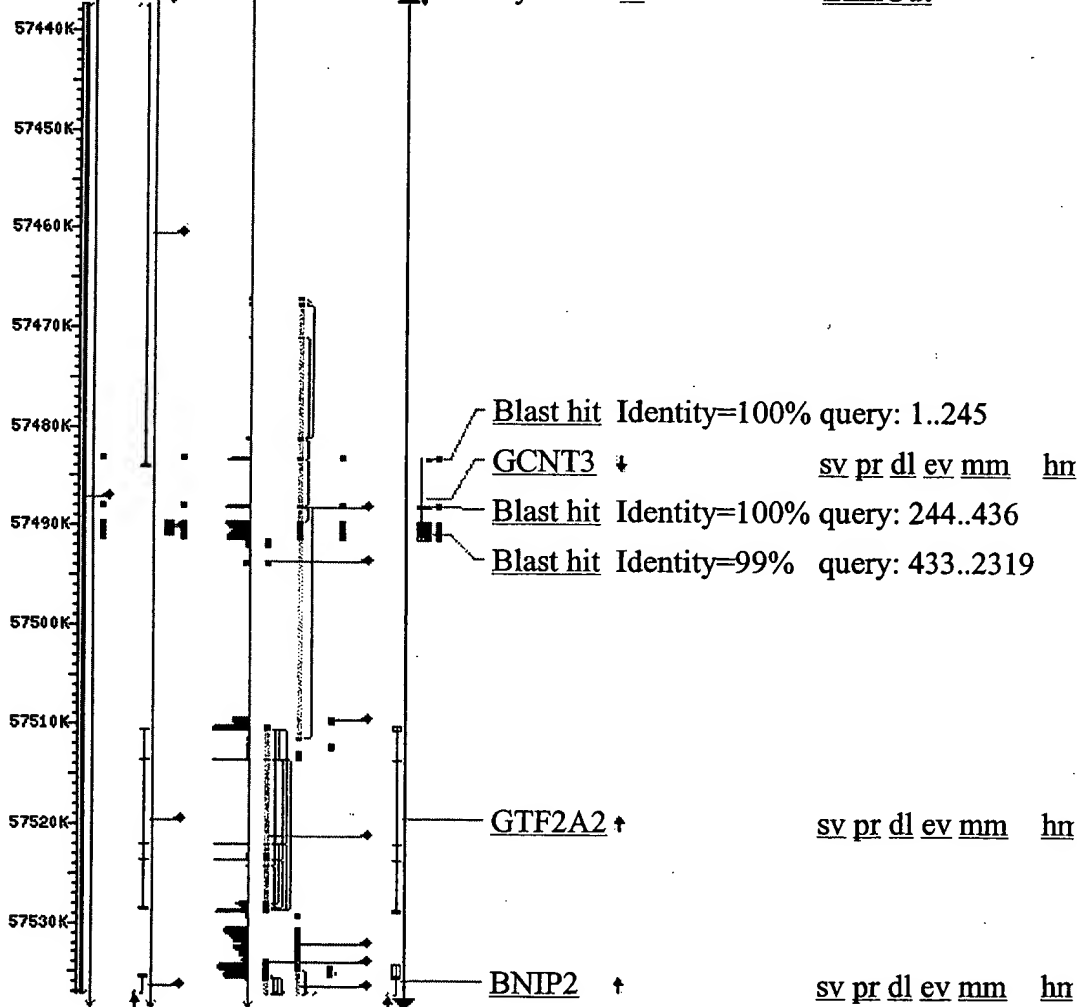
 Chromosome: [1](#) [2](#) [3](#) [4](#) [5](#) [6](#) [7](#) [8](#) [9](#) [10](#) [11](#) [12](#) [13](#) [14](#) [[15](#)] [16](#) [17](#) [18](#) [19](#) [20](#)  
[21](#) [22](#) [X](#) [Y](#)
Query: [BLAST](#): (2319 letters) [\[clear\]](#)

Color Key for Alignment Scores: &lt;40 40-50 50-80 80-200 &gt;=200

Master Map: Genes On Sequence

[Maps & Options](#)
Total Genes On Chromosome: **1206** [8 not localized]Region Displayed: **57,437K-57,537K bp**
[Download Sequence/View Evidence](#)
Genes Labeled: **6** Total Genes in Region: **6**

Contig	GScan	HsUniG	Gene...	Symbol	O
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results of **BLAST**

[illegible]

BLASTN 2.2.6 [Apr-09-2003]

RID: 1058796829-25315-29548.BLASTQ1

Database: contig

545 sequences; 2,866,452,029 total letters



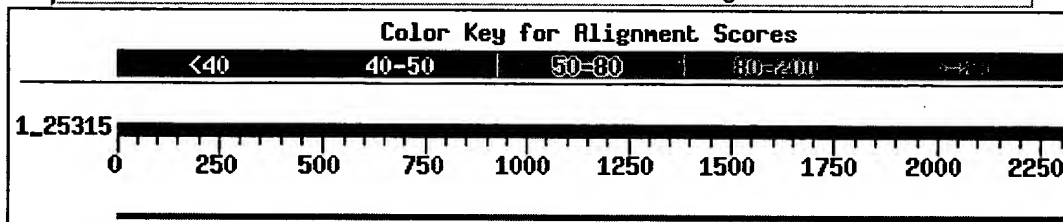
Show positions of the BLAST hits in the human genome using the Entrez Genomes MapViewer

**Query=**

(2319 letters)

### Distribution of 3 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:					Score	E
					(bits)	Value
ref NT_010194.15	Hs15_10351	Homo sapiens chromosome 15 geno...			3617	0.0

## Alignments

```
>ref|NT_010194.15|Hs15_10351 Homo sapiens chromosome 15 genomic contig
      Length = 53614549
```

Score = 3617 bits (1881), Expect = 0.0  
Identities = 1885/1887 (99%)  
Strand = Plus / Plus

Query: 433 aaggattgtgtcctcctccaccttccctgtgctcggctctccacctgtctcccattctgtg 492

|||||  
Sbjct: 30699986 aaggattgtgtcctcctccaccttcctgtgctcggtctccacctgtctccattctgtg 3070004

Query: 493 acgatgggttcaatggaagagactctgccagctgcattacttgtgggctctgggctgctat 552  
|||||  
Sbjct: 30700046 acgatgggttcaatggaagagactctgccagctgcattacttgtgggctctgggctgctat 3070010

Query: 553 atgctgctggccactgtggctctgaaactttctttcaggttgaagtgtgactctgaccac 612  
|||||  
Sbjct: 30700106 atgctgctggccactgtggctctgaaactttctttcaggttgaagtgtgactctgaccac 3070016

Query: 613 ttgggtctggagtcagggaatctcaaagccagtactgttaggaatatcttgataatttc 672  
|||||  
Sbjct: 30700166 ttgggtctggagtcagggaatctcaaagccagtactgttaggaatatcttgataatttc 3070022

Query: 673 ctgaaacttcagcaaagaggtctatcaactgttcaggggtcacccgaggggaccaagag 732  
|||||  
Sbjct: 30700226 ctgaaacttcagcaaagaggtctatcaactgttcaggggtcacccgaggggaccaagag 3070028

Query: 733 gcagtgttcaggctattctgaataacctggaggtcaagaagaagcgagagcctttcaca 792  
|||||  
Sbjct: 30700286 gcagtgttcaggctattctgaataacctggaggtcaagaagaagcgagagcctttcaca 3070034

Query: 793 gacaccactacctctccctcaccagagactgtgagcacttcaaggctgaaaggaagttc 852  
|||||  
Sbjct: 30700346 gacaccactacctctccctcaccagagactgtgagcacttcaaggctgaaaggaagttc 3070040

Query: 853 atacagttcccactgagcaaagaagaggtggagttccctattgcatactctatggtgatt 912  
|||||  
Sbjct: 30700406 atacagttcccactgagcaaagaagaggtggagttccctattgcatactctatggtgatt 3070046

Query: 913 catgagaagattgaaaactttgaaaggctactgagagctgtgtatgccctcagaacata 972  
|||||  
Sbjct: 30700466 catgagaagattgaaaactttgaaaggctactgagagctgtgtatgccctcagaacata 3070052

Query: 973 tactgtgtccatgtggatgagaagtcccagaaaactttcaaagaggcgggtcaaagcaatt 1032  
|||||  
Sbjct: 30700526 tactgtgtccatgtggatgagaagtcccagaaaactttcaaagaggcgggtcaaagcaatt 3070058

Query: 1033 atttcttgcttcccaaatgtcttcatagccagtaagctgggttcgggtgggttatgcctcc 1092  
|||||  
Sbjct: 30700586 atttcttgcttcccaaatgtcttcatagccagtaagctgggttcgggtgggttatgcctcc 3070064

Query: 1093 tgggtccagggtgcaagctgacctcaactgcatggaagacttgctccagagctcagtgccg 1152  
|||||  
Sbjct: 30700646 tgggtccagggtgcaagctgacctcaactgcatggaagacttgctccagagctcagtgccg 3070070

Query: 1153 tggaaatacttctgaatacatgtgggacggactttcctataaagagcaatgcagagatg 1212

|||||  
Sbjct: 30700706 tggaaatacttcctgaatacatgtgggacggactttcctataaagagcaatgcagagatg 3070076

Query: 1213 gtccaggctctcaagatgttgaatgggaggaatagcatggagtcagagggtacctcctaag 1272  
|||||  
Sbjct: 30700766 gtccaggctctcaagatgttgaatgggaggaatagcatggagtcagagggtacctcctaag 3070082

Query: 1273 cacaaagaaacccgctggaaatatcactttgaggtagtggagagacacattacacctaacc 1332  
|||||  
Sbjct: 30700826 cacaaagaaacccgctggaaatatcactttgaggtagtggagagacacattacacctaacc 3070088

Query: 1333 aacaagaagaaggatcctcccccttataatttaactatgtttacaggggaatgcgtacatt 1392  
|||||  
Sbjct: 30700886 aacaagaagaaggatcctcccccttataatttaactatgtttacaggggaatgcgtacatt 3070094

Query: 1393 gtggcttcccgagatttcgtccaacatgttttgaagaaccctaaatcccaacaactgatt 1452  
|||||  
Sbjct: 30700946 gtggcttcccgagatttcgtccaacatgttttgaagaaccctaaatcccaacaactgatt 3070100

Query: 1453 gaatgggtaaaagacacttatagcccagatgaacacctctggggccacccttcagcgtgca 1512  
|||||  
Sbjct: 30701006 gaatgggtaaaagacacttatagcccagatgaacacctctggggccacccttcagcgtgca 3070106

Query: 1513 cgggtggatgcctggctctgttcccaaccaccccaagtagcacatctcagacatgacttct 1572  
|||||  
Sbjct: 30701066 cgggtggatgcctggctctgttcccaaccaccccaagtagcacatctcagacatgacttct 3070112

Query: 1573 attgccaggctggtcaagtggcaggggtcatgagggagacatcgataaggggtgctccttat 1632  
|||||  
Sbjct: 30701126 attgccaggctggtcaagtggcaggggtcatgagggagacatcgataaggggtgctccttat 3070118

Query: 1633 gctccctgctctggaatccaccagcgggctatctgcgtttatggggctggggacttgaat 1692  
|||||  
Sbjct: 30701186 gctccctgctctggaatccaccagcgggctatctgcgtttatggggctggggacttgaat 3070124

Query: 1693 tggatgcttcaaaaccatcacctgttggccaacaagtttgacccaaaggtagatgataat 1752  
|||||  
Sbjct: 30701246 tggatgcttcaaaaccatcacctgttggccaacaagtttgacccaaaggtagatgataat 3070130

Query: 1753 gctcttcagtgccttagaagaatacctacgttataaggccatctatgggactgaactttga 1812  
|||||  
Sbjct: 30701306 gctcttcagtgccttagaagaatacctacgttataaggccatctatgggactgaactttga 3070136

Query: 1813 gacacactatgagagcggttgctacctgtggggcaagagcatgtacaaacatgctcagaac 1872  
|||||  
Sbjct: 30701366 gacacactatgagagcggttgctacctgtggggcaagagcatgtacaaacatgctcagaac 3070142

Query: 1873 ttgctgggacagtgtgggtgggagaccagggctttgcaattcgtggcatcctttaggata 1932

|||||  
Sbjct: 30701426 ttgctgggacagtgtgggtgggagaccagggctttgcaattcgtggcatccttaggata 3070148

Query: 1933 agagggctgctattagattgtgggtaagtagatctttgccttgcaaattgctgcctggg 1992  
|||||  
Sbjct: 30701486 agagggctgctattagagtgtgggtaagtagatctttgccttgcaaattgctgcctggg 3070154

Query: 1993 tgaatgctgcttgttctctcaccctaaccctagtagttcctccactaactttctcacta 2052  
|||||  
Sbjct: 30701546 tgaatgctgcttgttctctcaccctaaccctagtagttcctccactaactttctcacta 3070160

Query: 2053 agtgagaatgagaactgctgtgataggagagtgaaggagggatatgtggtagagcactt 2112  
|||||  
Sbjct: 30701606 agtgagaatgagaactgctgtgataggagagtgaaggagggatatgtggtagagcactt 3070166

Query: 2113 gatttcagttgaatgctgctggtagcttttccattctgtggagctgccgttcctaataa 2172  
|||||  
Sbjct: 30701666 gatttcagttgaatgctgctggtagcttttccattctgtggagctgccgttcctaataa 3070172

Query: 2173 ttccagggttggttagcgtggaggagaactttgatggaaagagaaccttcccttctgtact 2232  
|||||  
Sbjct: 30701726 ttccagggttggttagcgtggaggagaactttgatggaaagagaaccttcccttctgtact 3070178

Query: 2233 gttaacttaaaaataaataagctcctgattcaaagtattacctctacttttgcctagtat 2292  
|||||  
Sbjct: 30701786 gttaacttaaaaataaataagctcctgattcaaagtattacctctacttttgcctagtat 3070184

Query: 2293 gccagaaataatataaatctaaacaga 2319  
|||||  
Sbjct: 30701846 gccagaaataatataaatctaaacaga 30701872

Score = 471 bits (245), Expect = e-130  
Identities = 245/245 (100%)  
Strand = Plus / Plus

Query: 1 attaactgggttttctatttatctatcctctcgcattacttctctgagtcagagcctct 60  
|||||  
Sbjct: 30693547 attaactgggttttctatttatctatcctctcgcattacttctctgagtcagagcctct 3069360

Query: 61 tctctctaagtcacgggaactgcccttgctacttgtgacctgccctttactcagcagttt 120  
|||||  
Sbjct: 30693607 tctctctaagtcacgggaactgcccttgctacttgtgacctgccctttactcagcagttt 3069366

Query: 121 ttgttctgggaagccctgggattctgctaatacctatcactgtaggtgctgaagggaac 180  
|||||  
Sbjct: 30693667 ttgttctgggaagccctgggattctgctaatacctatcactgtaggtgctgaagggaac 3069372

Query: 181 agatgaagaacatgacctcaaggagcttcctgtcaatgagaagaccaagctgacgcctgg 240  
|||||  
Sbjct: 30693727 agatgaagaacatgacctcaaggagcttcctgtcaatgagaagaccaagctgacgcctgg 3069378

Query: 241 caaag 245  
|||||  
Sbjct: 30693787 caaag 30693791

Score = 371 bits (193), Expect = e-100  
Identities = 193/193 (100%)  
Strand = Plus / Plus

Query: 244 agatattaaagaggagcctgaaactgttccttgacatcttatgaatgtcagaaaatacc 303  
|||||  
Sbjct: 30698500 agatattaaagaggagcctgaaactgttccttgacatcttatgaatgtcagaaaatacc 3069855

Query: 304 ttttggagggttagaagatcaggggacatggttggttcacatttgctgccacggaacaccg 363  
|||||  
Sbjct: 30698560 ttttggagggttagaagatcaggggacatggttggttcacatttgctgccacggaacaccg 3069861

Query: 364 ccagtcttcacttggaacagaatcacgccttggaagagatcatccctaagcaggagag 423  
|||||  
Sbjct: 30698620 ccagtcttcacttggaacagaatcacgccttggaagagatcatccctaagcaggagag 3069867

Query: 424 aagctactaaagg 436  
|||||  
Sbjct: 30698680 aagctactaaagg 30698692

Database: contig  
Posted date: Apr 29, 2003 9:34 AM  
Number of letters in database: -1,428,515,263  
Number of sequences in database: 545

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2  
Gap Penalties: Existence: 0, Extension: 0  
Number of Hits to DB: 43,335  
Number of Sequences: 545  
Number of extensions: 0  
Number of successful extensions: 0  
Number of sequences better than 1.0e-02: 0  
Number of HSP's better than 0.0 without gapping: 0

Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 0  
length of query: 2319  
length of database: 2,866,452,029  
effective HSP length: 25  
effective length of query: 2294  
effective length of database: 2,866,438,404  
effective search space: 6575609698776  
effective search space used: 0  
S2: 26 (50.7 bits)